

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 25, 2004, 02:27:18 ; Search time 85 Seconds
(without alignments)
4839.873 Million cell updates/sec

Title: NP000123

Perfect score: 7803

Sequence: 1 MQELSTCFPLCLLRFCFSA.....WHQIALRMEVLCGEAQDLY 1456

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_29Jan04:*

1: Geneseq1980s:*

2: Geneseq1990s:*

3: Geneseq2000s:*

4: Geneseq2001s:*

5: Geneseq2002s:*

6: Geneseq2003as:*

7: Geneseq2003bs:*

8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7619.5	97.6	1661	2 AAW18670	AAW18670 Factor VII
2	7577.5	97.1	1471	4 AAB67959	Aab67959 Amino aci
3	7565.5	97.0	1471	2 AAW23414	Aaw23414 Human B-d
4	7535.5	96.6	1459	4 AAE10832	Aae10832 Human fac
5	7525.5	96.4	1459	4 AAE10833	Aae10833 Human fac
6	7522.5	96.4	1459	4 AAE10827	Aae10827 Human fac
7	7520.5	96.4	1457	2 AAW46246	Aaw46246 Human fac
8	7520.5	96.4	1457	2 AAW44372	Aaw44372 Human fac
9	7510.5	96.3	1447	5 ABG92541	Abg92541 5Arg B-do
10	7508.5	96.2	1457	2 AAY21675	Aay21675 Beta-doma
11	7501.5	96.1	1445	5 ABG32540	Abg32540 LE B-doma
12	7412.5	95.0	1424	4 AAB48842	Aab48842 Mutant ma
13	7412.5	95.0	1424	5 AAO18622	Aao18622 Human mat
14	7407.5	94.9	1438	3 AAB01262	Aab01262 B-domain
15	7401.5	94.9	1425	1 AAP80267	Aap80267 Modified
16	7398.5	94.8	1424	1 AAP80268	Aap80268 Modified
17	7394.5	94.8	1424	1 AAP91169	Aap91169 Sequence
18	7392	94.7	1440	2 AAR12971	Aar12971 Factor VI
19	7362	94.3	1516	1 AAP80265	Aap80265 Modified
20	7340	94.1	2342	2 AAW11422	AAW11422 Active Fa
21	7339	94.1	2344	2 AAW11432	AAW11432 Active Fa
22	7338.5	94.0	2345	2 AAW11453	AAW11453 Active Fa
23	7338.5	94.0	2345	2 AAW11441	AAW11441 Active Fa
24	7338.5	94.0	2345	2 AAW11446	AAW11446 Active Fa
25	7338	94.0	2346	2 AAW11434	AAW11434 Active Fa

26	7338	94.0	2346	2 AAW11421	AAW11421 Active Fa
27	7338	94.0	2346	2 AAW11452	AAW11452 Active Fa
28	7338	94.0	2346	2 AAW11431	AAW11431 Active Fa
29	7337	94.0	2348	2 AAW11436	AAW11436 Active Fa
30	7337	94.0	2348	2 AAW11449	AAW11449 Active Fa
31	7337	94.0	2348	2 AAW11448	AAW11448 Active Fa
32	7337	94.0	2348	2 AAW11444	AAW11444 Active Fa
33	7336.5	94.0	2349	2 AAW11420	AAW11420 Active Fa
34	7336.5	94.0	2349	2 AAW11440	AAW11440 Active Fa
35	7336.5	94.0	2349	2 AAW11424	AAW11424 Active Fa
36	7336.5	94.0	2349	2 AAW11428	AAW11428 Active Fa
37	7336.5	94.0	2349	2 AAW11430	AAW11430 Active Fa
38	7336.5	94.0	2349	2 AAW11443	AAW11443 Active Fa
39	7335.5	94.0	2351	1 AAP50059	Aap50059 Human fac
40	7335.5	94.0	2351	2 AAW11427	AAW11427 Active Fa
41	7335.5	94.0	2351	2 AAW11445	AAW11445 Active Fa
42	7335.5	94.0	2351	2 AAW11425	AAW11425 Active Fa
43	7335.5	94.0	2351	2 AAW11437	AAW11437 Active Fa
44	7335.5	94.0	2351	2 AAW11329	AAW11329 Native Fa
45	7335.5	94.0	2351	2 AAW11435	AAW11435 Active Fa

ALIGNMENTS

RESULT 1

AAW18670

ID AAW18670 standard; protein; 1661 AA.

XX AC AAW18670;

XX DT 10-AUG-1997 (first entry)

XX DE Factor VIII-dB695-HCII.

XX KW Factor VIII-dB695-HCII; heparin cofactor II; blood coagulation;

XX KW blood clotting; procoagulant; anticoagulant; antithrombotic; haemophilia;

XX KW gene therapy.

XX OS Homo sapiens.

XX FH Key

XX Domain

XX Location/Qualifiers

XX 731..760

XX /label= HCII

XX /note= "heparin cofactor II acidic domain"

XX FT

XX FT

XX FT

XX PN WO9718315-A1.

XX PD 22-MAY-1997.

XX PF 13-NOV-1996; 96WO-EP004977.

XX PR 13-NOV-1995; 95US-00558107.

XX XX (IMMO) IMMUNO AG.

XX PI Voorberg JJ;

XX XX WPI; 1997-289291/26.

XX DR N-PSDB; AAT69811.

XX PT Hybrid Factor VII with modified activity, comprises region from donor

XX PT anticoagulant or antithrombotic protein - useful for treatment of

XX PT coagulation disorders.

XX XX Claim 11; Page 52-60; 96pp; English.

XX CC Factor VIII-dB695-HCII (AAW18670) is a hybrid protein in which amino

XX CC acids 712-736 of Factor-dB695 (Factor VII del868-1562) B-domain are

XX CC replaced by amino acids 51-80 from the acidic region (and potential

XX CC thrombin-binding site) of human heparin cofactor II (HCII). It is the

XX CC expression product of Factor VIII-dB695-HCII DNA (AAT69811) in plasmid

XX CC pCLB-dB695-HCII. The hybrid protein, which can be expressed using gene

CC therapy techniques, has increased procoagulant activity owing to the HCII
 CC acidic region, and can be used to treat blood coagulation disorders such
 CC as haemophilia A
 XX
 SQ Sequence 1661 AA;

Query Match 97.6%; Score 7619.5; DB 2; Length 1661;
 Best Local Similarity 87.2%; Pred. No. 0;
 Matches 1449; Conservative 2; Mismatches 5; Indels 205; Gaps 4;

QY 1 MQIELSTCFCLLRFCSATRRYYLGAVELSWDMQSDLGELPVDARFPFRVPKSPFFN 60
 DB 1 MEIELSTCFCLLRFCSATRRYYLGAVELSWDMQSDLGELPVDARFPFRVPKSPFFN 60

QY 61 TSVVYKTLFVEFDHLENIAKPRPPWMLGGLPTQAEVDTVITLKNMASHPVSLHAV 120
 DB 61 TSVVYKTLFVEFDHLENIAKPRPPWMLGGLPTQAEVDTVITLKNMASHPVSLHAV 120

QY 121 GVSTWKASGEAYDDQTSQREKDDKVPFGSHTYVMQVLKENGPMASDPLCLTYSYLH 180
 DB 121 GVSTWKASGEAYDDQTSQREKDDKVPFGSHTYVMQVLKENGPMASDPLCLTYSYLH 180

QY 181 VDLVKDLSGLIGALLVCREGLAKETQTLHKILLFAVDEKSWHSETKNSLMQDRD 240
 DB 181 VDLVKDLSGLIGALLVCREGLAKETQTLHKILLFAVDEKSWHSETKNSLMQDRD 240

QY 241 AASARAWPKMTVNGYNRSLPGLIGCHRKSVYWHVIGMTTPVHSHIFLEGHTFLVRNH 300
 DB 241 AASARAWPKMTVNGYNRSLPGLIGCHRKSVYWHVIGMTTPVHSHIFLEGHTFLVRNH 300

QY 301 ROASLEISPIFTLTAQTLMDLQGLFLFCHISSHQHDMGEAYKVVDSCPEEPQLRMKNE 360
 DB 301 ROASLEISPIFTLTAQTLMDLQGLFLFCHISSHQHDMGEAYKVVDSCPEEPQLRMKNE 360

QY 361 EADYDDDLTDEMDVVRFDNDSPSFIQIRSVAKHPKTVWHVIAAEBEDWDYAPLVLA 420
 DB 361 EADYDDDLTDEMDVVRFDNDSPSFIQIRSVAKHPKTVWHVIAAEBEDWDYAPLVLA 420

QY 421 PDRSYKSYQLNNGPQIRGRYKVRFWAYTDEFKTRAIQHESGILGPLLXGEVGDTL 480
 DB 421 PDRSYKSYQLNNGPQIRGRYKVRFWAYTDEFKTRAIQHESGILGPLLXGEVGDTL 480

QY 481 LIIPKQASRPYNTYPHIGTIDVRPLYSRRLPKGVKHLKDFPILPGEIFYKWTVTEDGP 540
 DB 481 LIIPKQASRPYNTYPHIGTIDVRPLYSRRLPKGVKHLKDFPILPGEIFYKWTVTEDGP 540

QY 541 TKSDPRCLTRYSSFYVNERDLASGLIGPLLI CYKESVDORGQIMSDKNVILFSVFE 600
 DB 541 TKSDPRCLTRYSSFYVNERDLASGLIGPLLI CYKESVDORGQIMSDKNVILFSVFE 600

QY 601 NRSWYLTENIORPLNPAGVQLEDPEFOASINMHSINGYVFDLSQLSVCLHEVAYWYILS 660
 DB 601 NRSWYLTENIORPLNPAGVQLEDPEFOASINMHSINGYVFDLSQLSVCLHEVAYWYILS 660

QY 661 IGAQTDPLSVFFSGYTFKHKVVEDTLTLFPFSGETVFMENPGLMWILGCHNSDFNRG 720
 DB 661 IGAQTDPLSVFFSGYTFKHKVVEDTLTLFPFSGETVFMENPGLMWILGCHNSDFNRG 720

QY 721 MTALLKVS---DKNTGDI-----YED-----SFSQNRHPSSTKQKF 756
 DB 721 MTALLKVS---DKNTGDI-----YED-----SFSQNRHPSSTKQKF 756

QY 757 NATTIPENDIEKTPDFAHRTMPKIONVSSDLMLL----- 794
 DB 757 NATTIPENDIEKTPDFAHRTMPKIONVSSDLMLL----- 794

QY 795 ----- 794
 DB 795 ----- 794

QY 841 SDDPSGCAIDNNSLSBTHFRPQLHSGDMVFTPESGQLRLNEKLGTTADPLANDNH 900
 DB 841 SDDPSGCAIDNNSLSBTHFRPQLHSGDMVFTPESGQLRLNEKLGTTADPLANDNH 900

QY 901 GTQIPKEWKSQEKSPKTAFFKDKDTLSLNACESNHAIAAINEGONKPEIEVTWAKQGR 960
 DB 901 GTQIPKEWKSQEKSPKTAFFKDKDTLSLNACESNHAIAAINEGONKPEIEVTWAKQGR 960

QY 795 -----EMKKEDFDIYDDENQSPRSF 815
 DB 961 TERLCSQNPVLKRHOREITRTTLOSDQBEIDYDDTISVEMKKEDFDIYDDENQSPRSF 1020

QY 816 QKTRHYFIAAVERLWDYGMSSSPHVLNRNAGSGVPQFKVVFQBFQSTQPLRYRGE 875
 DB 1021 QKTRHYFIAAVERLWDYGMSSSPHVLNRNAGSGVPQFKVVFQBFQSTQPLRYRGE 1080

QY 876 LNEHLGLLPYIRAEVEDNIMVTFRNQASRPYSFYSLSISYBEDQOQAEPRKNFVKPNE 935
 DB 1081 LNEHLGLLPYIRAEVEDNIMVTFRNQASRPYSFYSLSISYBEDQOQAEPRKNFVKPNE 1140

QY 936 TKTYFWKVOHMAPTKDEFDCKAWAYPSVDVLEKDVHSLIGPLLYCHNTNLNPAHGRQV 995
 DB 1141 TKTYFWKVOHMAPTKDEFDCKAWAYPSVDVLEKDVHSLIGPLLYCHNTNLNPAHGRQV 1200

QY 996 TVQEPALFTTIFDETKSWYFTENMERNCRAPCNIQMEDPTFKENYAFHAINGYIMDTLPG 1055
 DB 1201 TVQEPALFTTIFDETKSWYFTENMERNCRAPCNIQMEDPTFKENYAFHAINGYIMDTLPG 1260

QY 1056 LVMAQDQIRRWYLLSGNSNENIHSIHFSCHVTTRKKEEYKMAALYNLYPGVFETVEMLPS 1115
 DB 1261 LVMAQDQIRRWYLLSGNSNENIHSIHFSCHVTTRKKEEYKMAALYNLYPGVFETVEMLPS 1320

QY 1116 KAGIWRVECLIGEHLAGMSTLFLVYSNKCOTPLGMASGHIRDFOITASGOYGOWAPKLA 1175
 DB 1321 KAGIWRVECLIGEHLAGMSTLFLVYSNKCOTPLGMASGHIRDFOITASGOYGOWAPKLA 1380

QY 1176 RLHYSGSINAWSTKEPFSWIKVDLLAPMIIHGKITQGARQKFSLSYISOFIIMYSLDGKK 1235
 DB 1381 RLHYSGSINAWSTKEPFSWIKVDLLAPMIIHGKITQGARQKFSLSYISOFIIMYSLDGKK 1440

QY 1236 WQTYRGNSTGTLMVFFGNVDSGGIKHNPPIIARYIRLHPTHYSIRSLRMLMGCDL 1295
 DB 1441 WQTYRGNSTGTLMVFFGNVDSGGIKHNPPIIARYIRLHPTHYSIRSLRMLMGCDL 1500

QY 1296 NSCSWPLGMESKAIADAQITASSYFTNMPATWSKARLHLOGRSNAMRPVNNPKWLQ 1355
 DB 1501 NSCSWPLGMESKAIADAQITASSYFTNMPATWSKARLHLOGRSNAMRPVNNPKWLQ 1560

QY 1356 VDFQTKMKTGVTGTVGKSLTSMYKBEFLISSQDGHOWTLFFQNGKVKVFGQNDST 1415
 DB 1561 VDFQTKMKTGVTGTVGKSLTSMYKBEFLISSQDGHOWTLFFQNGKVKVFGQNDST 1620

QY 1416 PVNNSLDPLLRIRYRIHPQSWHQAIALRMEVLGCEAODLY 1456
 DB 1621 PVNNSLDPLLRIRYRIHPQSWHQAIALRMEVLGCEAODLY 1661

RESULT 2

AAB67959
 ID AAB67959 standard; protein; 1471 AA.

XX AAB67959;

XX AC (first entry)

XX 29-JUN-2001

XX Amino acid sequence of human B-domain deleted factor VIII.
 XX Adeno-associated virus vector; B-domain; factor VIII; haemophilia A;
 XX coagulation disorder.

XX Homo sapiens.

XX WO200127303-A1.

XX 19-APR-2001.

XX 12-OCT-2000; 2000WO-US028221.

XX 12-OCT-1999; 99US-0158780P.

XX